14-0/= 03

A31869-A 070050.1046 **PATENT**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant

Andrey Rzhetsky et al.

Serial No.

09/549,827

Examiner

Zhou, S.

Filed

April 14, 2000

Group Art Unit:

1631

For

TACE VER OS 2003 CONTER 1800/2800 GENE DISCOVERY THROUGH COMPARISONS OF NETWORKS OF

STRUCTURAL AND FUNCTIONAL RELATIONSHIPS AMONG

KNOWN GENES AND PROTEINS

INFORMATION DISCLOSURE STATEMENT

March 31, 2003

EXPRESS MAIL NO.: EU588992085US

Assistant Commissioner of Patents and Trademarks Washington, D.C. 20231

Dear Sir:

In accordance with 37 C.F.R. §1.56 and §1.97(c)(2), Applicants respectfully request that the references relating to the above-identified application listed herein in reverse chronological alphabetical order be considered and made of record in the U.S. Patent and Trademark Office.

- 1. Ballinger CA et al., 1999, "Identification of CHIP, a novel tetratricopeptide repeatcontaining protein that interacts with heat shock proteins and negatively regulates chaperone functions," Mol. Cell. Biol. 19:4535-4545.
- 2. Barabasi and Albert, 1999, "Emergence of scaling in random networks," Science **286**:509-512
- 3. Enright AJ et al., 1999, "Protein interaction maps for complete genomes based on gene fusion events," Nature 402:86-90;

- 4. Marcotte EM et al., 1999, "Detecting protein function and protein-protein interactions from genome sequences," *Science* 285:751-753;
- 5. Ruecknagel KP et al., 1999, Dihydrolipoamide S-Succinyltransferase Precursor, Accession XUBYSD (gi|2144399);
- 6. Bailey et al., 1998, "Analysis of EST-driven gene annotation in human genomic sequence," Genome Research 8:362-376;
- 7. Bono et al., 1998, "Reconstruction of amino acid biosynthesis pathways from the complete genome sequence," *Genome Res.* 8:203-210;
- 8. Friedman C et al., 1998, "Evaluating natural language processing," *Methods of Information in Medicine* 37:334-44;
- 9. Goto S et al., 1998, "LIGAND:chemical database for enzymes reactions," *Nucleic Acid Research* 14:591-599;
- 10. Grundy, 1998, "Homology detection via family pairwise search," *J. Computational Biology* 5:479-491;
- 11. Hu et al., 1998, "WD-40 repeat region regulates Apaf-1 self-association and procaspase-9 activation," *J. Biol. Chem.* 273:33489-33494;
- 12. Sonnhammer ELL et al., 1998, "Pfam:multiple sequence alignments and HMM profiles of protein domains," *Nucleic Acids Research* 26(1):320-322;
- Wu SK et al., 1998, "Molecular role for the Rab binding platform of guanine nucleotide dissociation inhibitor in endoplasmic reticulum to golgi transport," *J. Biol. Chem.* 273:26931-26938;
- 14. Yuan et al., 1998, "Towards detection of orthologues in sequence databases," *Bioinformatics* 14:285-289;
- 15. Altschul et al., 1997, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," *Nucleic Acids Research* 25:3389-3402;
- 16. Attwood TK et al., 1997, "The PRINTS database of protein fingerprints:a novel information resource for computational molecular biology," *J. Chem. Inf. Comput. Sci.* 37:417-424;
- 17. Cserzo M et al., 1997, "Prediction of transmembrane α-helices in prokaryotic membrane proteins: the dense alignment surface method," *Protein Engineering* 10:673-676;
- 18. Goto et al., 1997, "Organizing and computing metabolic pathway data in terms of binary relations," *Pac. Symp. Biocomput.* 2:175-186;

- 19. Grundy et al., 1997, "Hidden Markov model analysis of motifs in steroid dehydrogenases and their homologs," *Biochem Biophys. Res. Commun.* 231(3):760-766;
- **20.** Grundy WN et al., 1997, "Meta-MEME: motif-based hidden Markov models of protein families," *CABIOS* **13**:397-406;
- 21. Mushegian AR et al., 1997, "Positionally cloned human disease genes:patterns of evolutionary conservation and functional motifs," *Proc. Natl. Acad Sci. USA* 94:5831-5836;
- 22. Neuwald, 1997, "Extracting protein alignment models from the sequence database," *Nucleic Acids Research* 25:1665-1677;
- 23. Pearson, 1997, "Identifying distantly related protein sequences," CABIOS, 13:325-332;
- 24. Pena et al., 1997, "Stress-induced apoptosis and the sphingomyelin pathway," *Biochem Pharmacol.*, 53:615-621.
- 25. Rogers MA et al., 1997, "Sequences and differential expression of the three novel human type II hair keratins," *Differentiation* 61:187-194;
- 26. Selkov, E et al., 1997, "The metabolic pathway collection: an update," *Nucleic Acids Research* 25:37-38;
- 27. Sharkey et al., 1997, "Hox genes in evolution: protein surfaces and paralog groups," *TIG* 13:145-151;
- 28. Skvorak AB et al., 1997, "An ancient conserved gene expressed in the human inner ear: identification, expression analysis, and chromosome mapping of human and mouse antiquitin (ATQ1), Genomics 46:191-199;
- 29. Sonnhammer ELL et al., 1997, Pfam: A comprehensive database of protein domains families based on seed alignments, *Proteins Structure Function and Genetics* 28:405-420;
- 30. Tatusov RL et al., 1997, "A genomic perspective on protein families," Science 278:631-637
- 31. Boskovic J et al., 1996, Transcription Factor GRF10, Accession A25872 (gi|82888);
- 32. Bucher et al., 1996, "A flexible motif search technique based on generalized profiles," *Comput. Chem.*, 20:3-23.
- Felsenstein J, 1996, "Inferring phylogenies from protein sequence by parsimony, distance, and likelihood means," *Methods in Enzymology* **266**:418-427;

- 34. Gilks WR et al., eds., 1996, *Markov Chain Monte Carlo Practice*, Chapman & Hall/CRC, New York;
- 35. Gustafsson C et al., 1996, "Identification of new RNA modifying enzymes by iterative genome search using known modifying enzymes as probes," *Nucleic Acids Research* 24:3756-3762;
- Jain NL et al., 1996, "Identification of suspected tuberculosis patients based on natural language processing of chest radiograph reports," Proc. AMIA Annu Fall Symp 542-546;
- James CM et al., 1996, Cell Division Control Protein CDC43, Accession RGBY43 (gi|2144611);
- 38. Koonin EV et al., 1996, "Protein sequence comparison at sequence scale," *Methods in Enzymology* 266:295-323;
- Mathews S et al., 1996,"The phytochrome family in grasses (Poaceae): A phlogeny and evidence that grasses have a subset of the loci found in dicot angiosperms," *Mol. Biol. Evol.*, 13:1141-1150;
- 40. Miklos GLG, et al., 1996, "The role of the genome project in determining gene function: insights from model organisms," *Cell* 86:521-529;
- 41. Selkov et al., 1996, "The metabolic pathway collection from EMP: the enzymes and metabolic pathways database," *Nucleic Acids Research* 24:26-28;
- Wu CH et al., 1996, "Motif identification neural design for rapid and sensitive protein family search," *Comput. Appl. Biosci* 12:109-118;
- **43.** Bailey et al. 1995, "The value of prior knowledge in discovering motifs," *Proc. Int Conf Intell Syst Biol.* **3**:21-29;
- 44. Boldin et al., 1995, "A novel protein that interacts with the death domain of Fas./APO1 contains a sequence motif related to the death domain," *J Biol Chem*, **270**:7795-8.
- 45. Friedman et al., 1995, "Natural language processing in an operational clinical information system," *Natural Language Engineering*, 1:83-108.
- 46. Green PJ, 1995, "Reversible Markov chain Monte Carlo computation and Bayesian model determination," *Biometrika* 82:711-732;
- 47. Hofmann et al., 1995, "The death domain motif found in Fas(Apo-1) and TNF receptor is present in proteins involved in apoptosis and axonal guidance," *FEBS Lett*, 371:321-3.
- 48. Hripcsak G et al., "Unlocking clinical data from narrative reports: a study of natural language processing," 1995, Ann. Intern Med. 122:681-688;

NY02:433879.1 - 4 -

- 49. Hurlin PJ., 1995, "Mad3 and Mad4:novel Max-interacting transcriptional repressors that suppress c-myc dependent transformation and are expressed during neural and epidermal differentiation," *EMBO* 14:5646-59.
- 50. Neuwald AF et al., 1995, "Gibbs motif sampling:detection of bacterial outer membrane protein repeats," *Protein Sci.* 4:1618-1632;
- 51. Purnelle B et al., 1995, Pre-mRNA Splicing Factor PRP21, Accession S23553 (gi|280467);
- 52. Yang Z et al., 1995, "Maximum likelihood trees from DNA sequences: A peculiar statistical estimation problem," *Syst. Biol.* 44:384-399;
- Zweigenbaum et al., 1995, "A multi-lingual architecture for building a normalised conceptual representation from medical language," *AMIA*, 357-361;
- 54. Claverie, 1994, "Some useful statistical properties of position-weight matrices," Comput. Chem., 18:287-94.
- 55. Churcher C, 1994, Dihydrolipoamide Dehydrogenase Precursor, Accession A30151 (gi|82983);
- 56. Contreras R et al., 1994, Hypothetical Protein YBL067C, Accession S45803 (gi|626480);
- 57. Entian KD et al., 1994, Omnipotent Suppressor Protein SUP45, Accession S46014 (gi|626763);
- 58. Gaillon L et al., 1994, Transcription Factor BAS1, Accession A40083 (gi|101447);
- 59. Hamlyn N et al., 1994, Oxoglutarate Dehydrogenase Precursor, Accession DEBY (gi|1070439);
- Kazic 1994, "Representation of biochemistry for modeling organisms," In: Molecular Modeling: From Virtual Tools to Real Problems, Kumosinski, T. and Liebman, M.N. (Eds.), American Chemical Society, Washington, D.C. pp. 486-494;
- 61. Kazic, 1994, "Biochemical databases: Challenges and opportunities," In: New Data Challenges in Our Information Age Glaesar, P.S. and Millward, M.T.L. (Eds.). Proceedings of the Thirteenth International CODATA Secretariat, Paris pp. C133-C140;
- Krogh et al., 1994, "Hidden Markov Models in computational biology, applications to protein modeling," *J. Mol. Biol.* **235**:1501-1531;
- 63. Lenert et al., 1994, "Automated linkage of free-text description of patients with a practice guideline," *AMIA*, 274-278;

- 64. Murphy L et al., 1994, Suppressor 2 Protein, Accession EFBY52 (gi|72877);
- 65. Rieger M, 1994, Protein Farnesyltransferase Chain RAM2, Accession P29703 (gi|266880);
- 66. Tatusov RL et al., 1994, "Detection of conserved segments in proteins: Iterative scanning of sequence databases with alignment blocks," *Proc. Natl Acad. Sci. USA* 91:12091-12095
- Orengo et al., 1993, "A local alignment method for protein structure motifs," *J Mol Biol* 233(3):488-497;
- 68. Ullrich O et al., 1993, "Rab GDP dissociation inhibitor as a general regulator for the membrane association of Rab proteins," *J. Biol. Chem.* 268:18143-18150;
- 69. Venezia, 1993, "Rapid motif compliance scoring with match weight sets," *Comput Appl Biosci*, 9:65-9.
- 70. Baud et al., 1992, "Natual language processing and semantical representation of medical texts," *Meth. Info. Med.*, 31:117-125;
- 71. Peitgen HO, Juregens H, Saupe D, 1992, Chaos and Fractals: New Frontiers of Science, Springer Verlag, New York;
- 72. Hirst et al., 1991, "Prediction of ATP-binding motifs: a comparison of a perceptron-type neural network and a consensus sequence method," *Prot Eng*, 4:615-623.
- 73. Altschul et al., 1990, "Basic local alignment search tool," J. Mol. Biol. 215:403-410;
- 74. Goldman N, 1990,"Maximum likelihood inference of phylogenetic trees, with special references to a poisson process model of DNA substitution and to parsimony analyses," *Syst. Zoo.* 39:345-361;
- 75. Haug et al., 1990, "Computerized extraction of coded findings from free-text radiologic reports," Radiology, 174:543-548;
- 76. Karlin S et al., 1990, "Methods for assessing the statistical significance of the molecular sequences features by using general scoring schemes," *Proc. Natl. Acad. Sci. USA* 87:2264-2268;
- 77. Pamilo P et al., 1988, "Relationship between gene tree and species trees," *Mol. Biol. Evol.* 5:568-583;
- 78. Saitou N, 1987, "The neighbor-joining method: A new method for reconstructing phylogenetic trees," *Mol. Biol. Evol.* 4:406-425;

- 79. Fitch WM, 1974, "Evolutionary trees with minimum nucleotide replacements from amino acid sequences," J. Mol. Evol. 3:263-278;
- 80. Felsenstein J, 1978, "Cases in which parsimony or compatibility methods will be positively misleading," *Syst. Zool.*, 27:401-410
- 81. Fitch WM, 1970, "Distinguishing homologous from analogous proteins," *Syst. Zool.*, 19:99-113; and
- **82.** Hastings, 1970, "Monte Carlo sampling methods using Markov chains and their applications," *Biometrika* **57**:97-109.

The referenced citations are listed in the accompanying PTO Form 1449. Copies of the references are submitted herewith in one bound volume.

References #34 and 71 are books, copies of which have not been provided to the Examiner with the present submission.

Identification of the references listed in the attached PTO Form 1449 is not to be construed as an admission of Applicants or Attorneys for Applicants that such references are available as "prior art" against the above-identified application.

NY02:433879.1 - 7 -

This Information Disclosure Statement is being filed before the mailing date of a final action under § 1.113, a notice of allowance under § 1.311, or an action that otherwise closes prosecution, and is accompanied by the fee set forth in 37 C.F.R. § 1.17(p). Please charge any additional required fees to Deposit Account No. 02-4377. Two copies of this page are enclosed.

Respectfully submitted,

Henry Tang

PTO Reg. No. 29,705

Lisa B. Kole

PTO Reg. No. 35,225

Carmella L. Stephens PTO Reg. No. 41,328

Attorney for Applicants BAKER BOTTS, L.L.P. 30 Rockefeller Plaza New York, NY 10112 (212) 408-2628

Enclosures

NY02:433879.1 - 8 -

This Information Disclosure Statement is being filed before the mailing date of a final action under § 1.113, a notice of allowance under § 1.311, or an action that otherwise closes prosecution, and is accompanied by the fee set forth in 37 C.F.R. § 1.17(p). Please charge any additional required fees to Deposit Account No. 02-4377. Two copies of this page are enclosed.

Respectfully submitted,

Henry Tang

PTO Reg. No. 29,705

Lisa B. Kole

PTO Reg. No. 35,225

Carmella L. Stephens PTO Reg. No. 41,328

Attorney for Applicants BAKER BOTTS, L.L.P. 30 Rockefeller Plaza New York, NY 10112 (212) 408-2628

Enclosures

This Information Disclosure Statement is being filed before the mailing date of a final action under § 1.113, a notice of allowance under § 1.311, or an action that otherwise closes prosecution, and is accompanied by the fee set forth in 37 C.F.R. § 1.17(p). Please charge any additional required fees to Deposit Account No. 02-4377. Two copies of this page are enclosed.

Respectfully submitted,

Mr J. Styluns Henry Tang

PTO Reg. No. 29,705

Lisa B. Kole PTO Reg. No. 35,225

Carmella L. Stephens PTO Reg. No. 41,328

Attorney for Applicants BAKER BOTTS, L.L.P. 30 Rockefeller Plaza New York, NY 10112 (212) 408-2628

Enclosures

Page	1	of	8
1 450		$\mathbf{v}_{\mathbf{I}}$	v

Form PTO-1449 U.S. Department of Commerce (REV. 2-82) Patent and Trademark Office

Ø	Atty.	Dock	et	No.
Я	4 2 1	0.00		070

A31869-A 070050.1046

Serial No. 09/549.827

INFORMATION DISCLOSURE STATEMENT BY APPLICANT

(Use several sheets if necessary)

Applicant Andrey Rzhetsky et al.

Filing Date
April 14, 2000

Group 1631

U.S. PATENT DOCUMENTS *Exam. Document No. Date Class Subclass Filing Date Name Init. ifAppropriate FOREIGN PATENT DOCUMENT **Translator** Document No. Date Country Class SubClass Yes No OTHER DOCUMENTS (including Author, Title Date, Pertinent Pages, Etc.) Ballinger CA et al., 1999, "Identification of CHIP, a novel tetratricopeptide repeat-containing protein that interacts with heat shock proteins and negatively regulates chaperone functions," Mol Cell. Biol. 19:4535-4545. Barabasi and Albert, 1999, "Emergence of scaling in random networks," Science 286:509-512. Enright AJ et al., 1999, "Protein interaction maps for complete genomes based on gene fusion events," Nature 402:86-90. Marcotte EM et al., 1999, "Detecting protein function and protein-protein interactions from genome sequences," Science 285:751-753. Ruecknagel KP et al., 1999, Dihydrolipoamide S-Succinyltransferase Precursor, Accession XUBYSD (gi|2144399)

NY02:433911.1

Examiner

Date Considered

^{*} Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not conformance and not considered. Include copy of this form with next communication to applicant.

Form PTO-1449 U.S. Department of Commerce
Patent and Trademark Office

Atty. Docket No. A31869-A 070050.1046

Serial No. 09/549,827

INFORMATION DISCLOSURE STATEMENT **BY APPLICANT**

(Use several sheets if necessary)

Applicant Andrey Rzhetsky et al.

Filing Date April 14, 2000 Group 1631

	Bailey et al., 1998, "Analysis of EST-driven gene annotation in human genomic sequence," Genome Research 8:362-376.
	Bono et al., 1998, "Reconstruction of amino acid biosynthesis pathways from the complete genome sequence," <i>Genome Res.</i> 8:203-210.
	Friedman C et al., 1998, "Evaluating natural language processing," <i>Methods of Information in Medicine</i> 37 :334-44.
	Goto S et al., 1998, "LIGAND:chemical database for enzymes reactions," <i>Nucleic Acid Research</i> 14:591-599.
* 886-1	Grundy, 1998, "Homology detection via family pairwise search," J. Computational Biology 5:479 491.
-	Hu et al., 1998, "WD-40 repeat region regulates Apaf-1 self-association and procaspase-9 activation," <i>J. Biol. Chem.</i> 273 :33489-33494.
	Sonnhammer ELL et al., 1998, "Pfam:multiple sequence alignments and HMM profiles of protein domains," <i>Nucleic Acids Research</i> 26 (1):320-322.
	Wu SK et al., 1998, "Molecular role for the Rab binding platform of guanine nucleotide dissociation inhibitor in endoplasmic reticulum to golgi transport," <i>J. Biol. Chem.</i> 273 :26931-26938.
	Yuan et al., 1998, "Towards detection of orthologues in sequence databases," <i>Bioinformatics</i> 14:285-289.
	Altschul et al., 1997, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," <i>Nucleic Acids Research</i> 25 :3389-3402.
	Attwood TK et al., 1997, "The PRINTS database of protein fingerprints:a novel information resource for computational molecular biology," <i>J. Chem. Inf. Comput. Sci.</i> 37:417-424.
	Cserzo M et al., 1997, "Prediction of transmembrane α-helices in prokaryotic membrane proteins: the dense alignment surface method," <i>Protein Engineering</i> 10:673-676.
	Goto et al., 1997, "Organizing and computing metabolic pathway data in terms of binary relations," <i>Pac. Symp. Biocomput.</i> 2:175-186.

NY02:433911.1

Examiner Date Considered

Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not conformance and not considered. Include copy of this form with next communication to applicant.

	, J .		
•			Page 3 of 8
Form PTO-1449 U.S. Department of Commerce (REV. 2-82) Patent and Trademark Office		Atty. Docket No. A31869-A 070050.1046	Serial No. 09/549,827
INFORMATION DISCLOSURE STATEMENT BY APPLICANT		Applicant Andrey Rzhetsky et al.	
OIPAU	se several sheets if necessary)	Filing Date Group April 14, 2000 1631	
MAR 3 1 2003 8			
RADEMARKO	Grundy et al., 1997, "Hidden Markov in homologs," <i>Biochem Biophys. Res. Co</i>		eroid dehydrogenases and thei
	Grundy WN et al., 1997, "Meta-MEM. CABIOS 13:397-406.	E: motif-based hidden Markov	models of protein families,"
	Mushegian AR et al., 1997, "Positiona conservation and functional motifs," Pr		
· · · · · · · · · · · · · · · · · · ·	Neuwald, 1997, "Extracting protein ali Research 25:1665-1677.	gnment models from the sequ	ence database," Nucleic Acids
	Pearson, 1997, "Identifying distantly re	elated protein sequences," CA	BIOS, 13:325-332;
	Pena et al., 1997, "Stress-induced apop <i>Pharmacol.</i> , 53 :615-621.	tosis and the sphingomyelin p	athway," <i>Biochem</i>
	Rogers MA et al., 1997, "Sequences an	nd differential expression of th	e three novel human type II

Selkov, E et al., 1997, "The metabolic pathway collection: an update," <i>Nucleic Acids Research</i> 25 :37-38.
Sharkey et al., 1997, "Hox genes in evolution: protein surfaces and paralog groups," <i>TIG</i> 13:145-151.
Skvorak AB et al., 1997, "An ancient conserved gene expressed in the human inner ear: identification, expression analysis, and chromosome mapping of human and mouse antiquitin (ATQ1), Genomics 46:191-199.

hair keratins," Differentiation 61:187-194.

Sonnhammer ELL et al., 1997, Pfam: A comprehensive database of protein domains families based on seed alignments, *Proteins Structure Function and Genetics* **28**:405-420.

NY02:433911.1

Th		
Examiner	Date Considered	

^{*} Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not conformance and not considered. Include copy of this form with next communication to applicant.

	Examiner Date Considered			
NY02:433911.1 Examiner	Date (Considered		
NIV02.4220111	Wu CH et al., 1996, "Motif identification search," Comput. Appl. Biosci 12:109-1		ensitive protein family	
	Selkov et al., 1996, "The metabolic pathway collection from EMP: the enzymes and metabolic pathways database," <i>Nucleic Acids Research</i> 24:26-28.			
	Miklos GLG, et al., 1996, "The role of the genome project in determining gene function:insights from model organisms," <i>Cell</i> 86:521-529.			
	Mathews S et al., 1996,"The phytochron that grasses have a subset of the loci for	me family in grasses (Poaceae): and in dicot angiosperms," Mol.	A phlogeny and evidence <i>Biol. Evol.</i> , 13 :1141-1150	
	Koonin EV et al., 1996, "Protein sequer 266 :295-323.	nce comparison at sequence sca	le," Methods in Enzymolog	
	James CM et al., 1996, Cell Division Co	ontrol Protein CDC43, Accession	on RGBY43 (gi 2144611).	
	Jain NL et al., 1996, "Identification of suspected tuberculosis patients based on natural language processing of chest radiograph reports," Proc. AMIA Annu Fall Symp 542-546.			
	Gustafsson C et al., 1996, "Identification of new RNA modifying enzymes by iterative genome search using known modifying enzymes as probes," <i>Nucleic Acids Research</i> 24 :3756-3762.			
	Gilks WR et al., eds., 1996, Markov Chain Monte Carlo Practice, Chapman & Hall/CRC, New York.			
	Felsenstein J, 1996, "Inferring phyloger likelihood means," <i>Methods in Enzymo</i>		parsimony, distance, and	
	Bucher et al., 1996, "A flexible motif so Chem., 20:3-23.	earch technique based on gener	alized profiles," Comput.	
RAPPMARKO	Boskovic J et al., 1996, Transcription Factor GRF10, Accession A25872 (gi 82888).			
MAR 3 2003	Tatusov RL et al., 1997, "A genomic perspective on protein families," Science 278:631-637.			
OIPE (Us	se several sheets if necessary)	Filing Date April 14, 2000	Group 1631	
INFORMATION DISCLOSURE STATEMENT BY APPLICANT		Applicant Andrey Rzhetsky et al.		
Form PTO-1449 U.S. Department of Commerce (REV. 2-82) Patent and Trademark Office A31869-A 070050.1046 Serial No. 09/549,827				

^{*} Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not conformance and not considered. Include copy of this form with next communication to applicant.

	·		1 450 3 01 0	
Form PTO-1449 (REV. 2-82) P	U.S. Department of Commerce atent and Fredemark Office	Atty. Docket No. A31869-A 070050.1046	Serial No. 09/549,827	
INFORMA'	TION DISCLOSURE STATEMENT BY APPLICANT	Applicant Andrey Rzhetsky et al.		
	e several sheets if necessary)	Filing Date Group April 14, 2000 1631		
3 1 2003				
Bailey et al. 1995, "The value of prior knowledge in discovering motifs," Proc. Int Conf Interest Biol. 3:21-29.			fs," Proc. Int Conf Intell Sys	
	Boldin et al., 1995, "A novel protein the sequence motif related to the death don			
	Friedman et al., 1995, "Natural language Natural Language Engineering, 1:83-1		clinical information system,	
	Green PJ, 1995, "Reversible Markov cl determination," <i>Biometrika</i> 82:711-73	nain Monte Carlo computation 2.	and Bayesian model	
	Hofmann et al., 1995, "The death domain motif found in Fas(Apo-1) and TNF receptor is present in proteins involved in apoptosis and axonal guidance," FEBS Lett, 371:321-3.			
	Hripcsak G et al., "Unlocking clinical of processing," 1995, Ann. Intern Med. 12		udy of natural language	
	Hurlin PJ., 1995, "Mad3 and Mad4:nov c-myc dependent transformation and ar <i>EMBO</i> 14:5646-59.	rel Max-interacting transcription e expressed during neural and e	nal repressors that suppress epidermal differentiation,"	
	Neuwald AF et al., 1995, "Gibbs motifs repeats," <i>Protein Sci.</i> 4:1618-1632.	sampling:detection of bacterial	outer membrane protein	
	Purnelle B et al., 1995, Pre-mRNA Spli	cing Factor PRP21, Accession	S23553 (gi 280467)	
	Yang Z et al., 1995, "Maximum likeliho estimation problem," Syst. Biol. 44:384	ood trees from DNA sequences -399.	: A peculiar statistical	
	Zweigenbaum et al., 1995, "A multi-lin representation from medical language,"	gual architecture for building a AMIA, 357-361	normalised conceptual	
NY02:433911.1				
Examiner	Date (Considered		

^{*} Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not conformance and not considered. Include copy of this form with next communication to applicant.

Form PTO-1449 U.S. Department of Commerce (REV. 2-82) Patent and Trademark Office A31869-A 070050.1046 Serial No. 09/549,827					
INFORMATION DISCLOSURE STATEMENT BY APPLICANT			Applicant Andrey Rzhetsky et al.		
OIP	(Use several sheets if necessary) Filing Date April 14, 2000 Group 1631			•	
	(Z)				
MAR 3	2003	Claverie, 1994, "Some useful statistica 18:287-94.	al properties of position-weight matrices," Comput. Chem.,		
CA TRAD	EMACE OF	Churcher C, 1994, Dihydrolipoamide Dehydrogenase Precursor, Accession A30151 (gi 82983)			
	-	Contreras R et al., 1994, Hypothetical l	Protein YBL067C, Accession S	45803 (gi 626480)	
		Entian KD et al., 1994, Omnipotent Su	ppressor Protein SUP45, Acces	sion S46014 (gi 626763)	
·		Gaillon L et al., 1994, Transcription Fa	ctor BAS1, Accession A40083	(gi 101447)	
		Hamlyn N et al., 1994, Oxoglutarate Do	ehydrogenase Precursor, Access	sion DEBY (gi 1070439)	
-		Kazic 1994, "Representation of biochemistry for modeling organisms," In: Molecular Modeling: From Virtual Tools to Real Problems, Kumosinski, T. and Liebman, M.N. (Eds.), American Chemical Society, Washington, D.C. pp. 486-494.			
		Kazic, 1994, "Biochemical databases:C Our Information Age Glaesar, P.S. and International CODATA Secretariat, Par	Millward, M.T.L. (Eds.). Proce	n: New Data Challenges in eedings of the Thirteenth	
	Krogh et al., 1994, "Hidden Markov Models in computational biology, applications to protein modeling," J. Mol. Biol. 235:1501-1531.				
	Lenert et al., 1994, "Automated linkage of free-text description of patients with a practice guideline," AMIA, 274-278.				
		Murphy L et al., 1994, Suppressor 2 Pro	otein, Accession EFBY52 (gi 72	2877)	
		Rieger M, 1994, Protein Farnesyltransfe	erase Chain RAM2, Accession	P29703 (gi 266880)	
		Tatusov RL et al., 1994, "Detection of consequence databases with alignment block	conserved segments in proteins: eks," Proc. Natl Acad. Sci. USA	Iterative scanning of 91 :12091-12095.	
NY02:43	3911.1	1			

Date Considered

Examiner

^{*} Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not conformance and not considered. Include copy of this form with next communication to applicant.

Form PTO-1449 U.S. Department of Commerce (REV. 2-82) Patent and Trademark Office

Atty. Docket No. A31869-A 070050.1046

Serial No. 09/549,827

INFORMATION DISCLOSURE STATEMENT BY APPLICANT

(Use several sheets if necessary)

Applicant Andrey Rzhetsky et al.

Filing Date Group
April 14, 2000 1631

TPE	7.pm 14, 2000
₹ 3 1 2003	Orengo et al., 1993, "A local alignment method for protein structure motifs," <i>J Mol Biol</i> 233 (3):488-497.
SADE ARE	Ullrich O et al., 1993, "Rab GDP dissociation inhibitor as a general regulator for the membrane association of Rab proteins," <i>J. Biol. Chem.</i> 268 :18143-18150.
	Venezia, 1993, "Rapid motif compliance scoring with match weight sets," <i>Comput Appl Biosci</i> , 9:65-9.
	Baud et al., 1992, "Natual language processing and semantical representation of medical texts," <i>Meth. Info. Med.</i> , 31:117-125.
- 22	Peitgen HO, Juregens H, Saupe D, 1992, Chaos and Fractals: New Frontiers of Science, Springer Verlag, New York
	Hirst et al., 1991, "Prediction of ATP-binding motifs:a comparison of a perceptron-type neural network and a consensus sequence method," <i>Prot Eng</i> , 4:615-623.
	Altschul et al., 1990, "Basic local alignment search tool," J. Mol. Biol. 215:403-410.
	Goldman N, 1990, "Maximum likelihood inference of phylogenetic trees, with special references to a poisson process model of DNA substitution and to parsimony analyses," Syst. Zoo. 39:345-361.
	Haug et al., 1990, "Computerized extraction of coded findings from free-text radiologic reports," Radiology, 174:543-548.
	Karlin S et al., 1990, "Methods for assessing the statistical significance of the molecular sequences features by using general scoring schemes," <i>Proc. Natl. Acad. Sci. USA</i> 87:2264-2268
	Pamilo P et al., 1988, "Relationship between gene tree and species trees," <i>Mol. Biol. Evol.</i> 5:568-583.
	Saitou N, 1987, "The neighbor-joining method: A new method for reconstructing phylogenetic trees," <i>Mol. Biol. Evol.</i> 4 :406-425.
	Fitch WM, 1974, " Evolutionary trees with minimum nucleotide replacements from amino acid sequences," J. Mol. Evol. 3:263-278.

NYU2:433911.1

Examiner Date Considered

^{*} Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not conformance and not considered. Include copy of this form with next communication to applicant.

Page 8	3 o	f :	8
--------	-----	-----	---

Form P	TO-1449	U.S. Dep	artment of	Commerce
(REV. 2	2-82) Pa	tent and	Trademark	Office

A31869-A 070050.1046 Applicant

Atty. Docket No.

Serial No. 09/549,827

INFORMATION DISCLOSURE STATEMENT BY APPLICANT

(Use several sheets if necessary)

Andrey Rzhetsky et al.

Filing Date April 14, 2000

Group 1631

Felsenstein J, 1978, "Cases in which parsimony or compatibility methods will be positively misleading," *Syst. Zool.*, 27:401-410.

Fitch WM, 1970, "Distinguishing homologous from analogous proteins," Syst. Zool., 19:99-113.

Hastings, 1970, "Monte Carlo sampling methods using Markov chains and their applications," *Biometrika* **57**:97-109.

NY02:433911.1

Examiner

Date Considered

^{*} Examiner: Initial citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not conformance and not considered. Include copy of this form with next communication to applicant.